2-20-2007

Supplementary Data for "Sequence and annotation of the 369-kb NY-2A and the 345-kb AR158 viruses that infect *Chlorella* NC64A": Appendix C: Gene Names c001R – c814L

Lisa A. Fitzgerald
University of Nebraska-Lincoln, lisa.fitzgerald@nrl.navy.mil

Michael V. Graves
University of Massachusetts–Lowell, Michael_Graves@uml.edu

Xiao Li
University of Massachusetts–Lowell

Tamara Feldblyum
The Institute for Genomic Research, Rockville, MD

William C. Nierman
The Institute for Genomic Research, Rockville, MD, wnierman@tigr.org

See next page for additional authors

Main article published in *Virology* 358:2 (February 20, 2007), pp. 472-484. doi:10.1016/j.virol.2006.08.033 Submitted July 27, 2006; revised August 17, 2006; accepted August 23, 2006; published online October 4, 2006.

SUPPLEMENTARY DATA FOR

Sequence and annotation of the 369-kb NY-2A and the 345-kb AR158 viruses that infect *Chlorella* NC64A

Lisa A. Fitzgerald[a], Michael V. Graves[b], Xiao Li[b], Tamara Feldblyum[c], William C. Nierman[c, d], and James L. Van Etten[e, *]

[a] Department of Chemistry, University of Nebraska-Lincoln, Lincoln, NE 68588-0304
[b] Department of Biological Sciences, University of Massachusetts-Lowell, Lowell, MA 01854
[c] The Institute for Genomic Research, 9712 Medical Center Drive, Rockville, MD 20850
[d] The George Washington University School of Medicine, Department of Biochemistry and Molecular Biology, Washington, DC 20037
[e] Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln, NE 68583-0722 and Nebraska Center for Virology, University of Nebraska-Lincoln, Lincoln, NE 68588-0666
* Corresponding author. Email: jvanetten@unlnotes.unl.edu

Abstract: Viruses NY-2A and AR158, members of the family *Phycodnaviridae*, genus *Chlorovirus*, infect the fresh water, unicellular, eukaryotic, chlorella-like green alga, *Chlorella* NC64A. The 368,683-bp genome of NY-2A and the 344,690-bp genome of AR158 are the two largest chlorella virus genomes sequenced to date; NY-2A contains 404 putative protein-encoding and 7 tRNA-encoding genes and AR158 contains 360 putative protein-encoding and 6 tRNA-encoding genes. The protein-encoding genes are almost evenly distributed on both strands, and intergenic space is minimal. Two of the NY-2A genes encode inteins, the large subunit of ribonucleotide reductase and a superfamily II helicase. These are the first inteins to be detected in the chlorella viruses. Approximately 40% of the viral gene products resemble entries in the public databases, including some that are unexpected for a virus. These include GDP-d-mannose dehydratase, fucose synthase, aspartate transcarbamylase, Ca^{++} transporting ATPase and ubiquitin. Comparison of NY-2A and AR158 protein-encoding genes with the prototype chlorella virus PBCV-1 indicates that 85% of the genes are present in all three viruses.

Keywords: Chlorella viruses, Phycodnaviridae, Virus NY-2A, Virus AR158, Genome sequence

Supplementary data associated with this article is archived in this repository as 4 separate files: Appendices A–D. Each document, in spreadsheet format, shows Gene Name, Genome Position, A.A. length, Peptide Mw, pI, CDD Hit Number, COGs, COG Definition, Bit Score, E-value, % Identity, % Positive, Query from-to, Hit from-to, BLASTp Hit Number, Hit Accession, BLASTp Definition, Bit Score, E-value, % Identity, % Positive, Query from-to, and Hit from-to.

Appendix A: Gene Names b002R – b797R
Appendix B: Gene Names B001L – B886R
Appendix C: Gene Names c001R – c814L
Appendix D: Gene Names C006R – C815L

Appendix C: Gene Names c001R – c814L

Gene Name	Genome Position	A.A. lenath	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to
c001R	858--1208	117	13,216	10.00		No Hit Found									No Hit Found								
c002L	1117--914	68	7,355	4.11		No Hit Found									No Hit Found								
c003L	1407--1162	82	9,208	5.03		No Hit Found									No Hit Found								
c004R	1345--1566	74	8,633	7.51		No Hit Found									No Hit Found								
c005L	2768--2553	72	7,560	6.39		No Hit Found									No Hit Found								
c007L	2853--2656	66	8,324	8.67		No Hit Found									No Hit Found								
c009R	4107--4307	67	8,180	7.70		No Hit Found									No Hit Found								
c010R	4195--4416	74	8,305	10.98		No Hit Found									No Hit Found								
c012R	4739--5137	133	14,851	10.74		No Hit Found									No Hit Found								
c013L	5249--4968	94	10,864	12.36		No Hit Found									No Hit Found								
c014L	6059--5835	75	9,020	11.14		No Hit Found									No Hit Found								
c016R	5923--6135	71	8,679	11.14		No Hit Found									No Hit Found								
c017R	6653--6874	74	8,908	7.95		No Hit Found									No Hit Found								
c019L	8506--8288	73	8,018	10.84		No Hit Found									No Hit Found								
c020L	8636--8364	91	10,668	4.74		No Hit Found									No Hit Found								
c022R	9629--9838	70	7,637	7.03		No Hit Found									No Hit Found								
c023R	10013--10267	85	9,780	7.03		No Hit Found									No Hit Found								
c025L	10493--10260	78	8,776	12.21		No Hit Found									No Hit Found								
c026R	10400--10885	162	15,129	6.51		No Hit Found									No Hit Found								
c027R	10482--10724	81	7,004	7.01		No Hit Found									No Hit Found								
c028L	11138--10896	81	9,300	9.03		No Hit Found									No Hit Found								
c030L	12030--11833	66	7,378	12.02		No Hit Found									No Hit Found								
c032L	12699--12505	65	7,548	11.07		No Hit Found									No Hit Found								
c033R	14085--14363	93	10,260	4.54		No Hit Found									No Hit Found								
c034R	14457--14663	69	7,533	4.11		No Hit Found									No Hit Found								
c035R	15405--15620	72	8,118	4.88		No Hit Found									No Hit Found								
c038L	20114--19836	93	10,815	11.75		No Hit Found									No Hit Found								
c039R	20154--20471	106	13,496	11.94		No Hit Found									No Hit Found								
c040R	20225--20644	140	15,363	6.44		No Hit Found									No Hit Found								
c041R	21263--21613	117	12,757	4.77		No Hit Found									No Hit Found								
c042R	21734--21976	81	8,902	4.36		No Hit Found									No Hit Found								
c043R	21986--22390	135	14,717	4.36		No Hit Found									No Hit Found								
c045R	23050--23385	112	12,025	3.86		No Hit Found									No Hit Found								
c046R	23722--23919	66	7,153	3.83		No Hit Found									No Hit Found								
c047R	24526--24927	134	15,178	5.19		No Hit Found									No Hit Found								
c049L	26322--26053	90	10,915	10.53		No Hit Found									No Hit Found								
c050L	27023--26817	69	8,732	10.36		No Hit Found									No Hit Found								
c053R	29160--29459	100	11,626	8.45		No Hit Found									No Hit Found								
c054R	30036--30260	75	8,463	6.50		No Hit Found									No Hit Found								
c058L	32400--32086	105	11,811	11.09		No Hit Found									No Hit Found								
c059R	32134--32358	75	9,266	8.65		No Hit Found								1	NP_048391	a43R	160.23	1.61E-38	92%	94%	1--75	1--75
c060L	32599--32345	85	9,926	7.79		No Hit Found								1	NP_048520	a172L	90.12	2.06E-17	49%	71%	4--85	4--86
c067R	36452--36772	107	12,931	8.17		No Hit Found								1	NP_048400	a52R	72.79	3.37E-12	88%	91%	39--74	1--36
c070L	37569--37273	99	11,285	8.46		No Hit Found									No Hit Found								
c071R	37404--37646	81	9,390	12.33		No Hit Found									No Hit Found								
c076R	40834--41088	85	9,619	10.52		No Hit Found									No Hit Found								
c077R	41317--41559	81	8,642	11.27		No Hit Found								1	NP_048874	a518R	82.42	4.19E-15	61%	66%	1--74	1--75
c079R	41856--42158	101	11,879	4.80		No Hit Found									No Hit Found								
c080R	42043--42243	67	7,428	11.66		No Hit Found									No Hit Found								
c082L	42700--42482	73	8,199	10.86		No Hit Found									No Hit Found								
c083L	42949--42734	72	7,961	11.22		No Hit Found									No Hit Found								
c084L	43118--42810	103	12,209	5.28		No Hit Found									No Hit Found								
c085R	42826--43095	90	10,283	12.37		No Hit Found									No Hit Found								
c087L	43830--43534	99	11,655	10.86		No Hit Found									No Hit Found								
c088L	44198--43725	158	18,278	6.91		No Hit Found								1	NP_048417	contains Gly-rich Gx motif LGGGLG (5X); contains type I hydrophobic tra	106.30	2.89E-22	60%	78%	77--158	1--82
c091R	45414--45683	90	10,722	12.10		No Hit Found									No Hit Found								
c092L	45973--45743	77	8,822	4.37		No Hit Found								1	NP_048503	a155R	88.20	7.74E-17	67%	81%	11--75	22--86
c094L	46498--46280	73	9,099	11.44		No Hit Found									No Hit Found								

Gene Name	Genome Position	A.A. lenath	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to
c095R	46384--46647	88	10,427	6.51		No Hit Found									No Hit Found								
c096R	46559--46783	75	8,714	11.72		No Hit Found									No Hit Found								
c099R	47348--47569	74	8,973	11.96		No Hit Found									No Hit Found								
c101L	47831--47637	65	7,735	11.80		No Hit Found								1	NP_048424	a76L	81.26	9.47E-15	59%	72%	7--65	29--103
c103R	48127--48393	89	10,619	9.04		No Hit Found									No Hit Found								
c105L	48553--48332	74	8,787	6.23		No Hit Found									No Hit Found								
c106R	48477--48920	148	16,988	12.25		No Hit Found									No Hit Found								
c107R	48667--49050	128	15,872	12.73		No Hit Found									No Hit Found								
c108L	49030--48701	110	12,147	4.53		No Hit Found									No Hit Found								
c109R	48951--49169	73	8,248	4.44		No Hit Found									No Hit Found								
c111L	50241--50035	69	7,818	7.69		No Hit Found									No Hit Found								
c113L	50991--50605	129	14,954	8.53		No Hit Found								1	NP_048428	a80L	83.19	2.45E-15	56%	73%	4--78	59--133
c113L														2	NP_048808	similar to PBCV-1 ORF a80L, encoded by GenBank Accession Number U	52.37	4.64E-06	55%	77%	1--45	56--100
c115R	51552--51854	101	11,969	5.03		No Hit Found									No Hit Found								
c117R	52181--52435	85	10,012	10.33		No Hit Found									No Hit Found								
c119L	53120--52878	81	9,832	10.44		No Hit Found									No Hit Found								
c120L	53301--53107	65	6,979	10.84		No Hit Found								1	NP_048434	a86L	115.16	5.92E-25	88%	91%	1--65	1--67
c122L	53809--53456	118	14,006	8.74		No Hit Found									No Hit Found								
c125R	54576--54854	93	10,295	6.27		No Hit Found									No Hit Found								
c127R	56008--56250	81	9,887	12.34		No Hit Found									No Hit Found								
c129L	57218--57024	65	6,945	11.08		No Hit Found									No Hit Found								
c130L	57627--57304	108	12,676	7.21		No Hit Found									No Hit Found								
c131L	58671--58321	117	13,915	7.33		No Hit Found									No Hit Found								
c133L	58873--58634	80	9,314	11.01		No Hit Found								1	NP_048449	a101L	80.49	1.60E-14	65%	87%	1--55	33--87
c135R	60778--60999	74	8,490	5.70		No Hit Found									No Hit Found								
c136L	62005--61682	108	12,746	11.14		No Hit Found									No Hit Found								
c138L	62271--62071	67	7,631	11.05		No Hit Found								1	NP_048450	a102L	74.71	8.81E-13	67%	70%	1--55	1--55
c139R	62218--62478	87	10,553	8.38		No Hit Found									No Hit Found								
c141R	63522--63800	93	10,443	9.04		No Hit Found									No Hit Found								
c144R	64162--64443	94	11,576	10.77		No Hit Found									No Hit Found								
c145R	64563--64808	82	10,093	8.66		No Hit Found									No Hit Found								
c147R	64964--65188	75	8,899	9.58		No Hit Found									No Hit Found								
c148L	65584--65348	79	9,420	9.90		No Hit Found									No Hit Found								
c149L	65751--65419	111	13,009	11.06		No Hit Found								1	NP_048458	a110L	178.72	4.30E-44	85%	89%	10--111	1--102
c151L	66402--66112	97	10,606	9.77		No Hit Found								1	NP_048460	a112L	191.05	8.51E-48	96%	96%	1--97	1--97
c152L	66829--66602	76	8,774	9.66		No Hit Found								1	NP_048463	a115L	97.44	1.28E-19	61%	68%	1--76	1--76
c153R	66732--66965	78	9,066	7.94		No Hit Found								1	NP_048464	a116R	105.15	6.10E-22	70%	75%	1--78	1--78
c154L	67618--67190	143	16,723	6.22		No Hit Found								1	NP_048465	a117L	177.56	9.63E-44	63%	80%	7--136	1--130
c156L	68903--68421	161	19,134	8.25		No Hit Found									No Hit Found								
c158L	69548--69270	93	10,616	7.09		No Hit Found									No Hit Found								
c159L	70317--69982	112	13,401	9.58		No Hit Found									No Hit Found								
c161L	70671--70441	77	8,834	6.50		No Hit Found									No Hit Found								
c163L	72952--71135	606	66,489	4.07		No Hit Found								1	XP_499823	hypothetical protein	53.53	2.42E-05	23%	36%	231--570	135--438
c164L	73444--73241	68	7,426	4.32		No Hit Found									No Hit Found								
c165L	74207--73557	217	25,658	10.46		No Hit Found									No Hit Found								
c166L	73876--73613	88	9,636	6.62		No Hit Found									No Hit Found								
c168L	75179--74985	65	7,619	11.13		No Hit Found								1	NP_048473	a124L	59.31	3.85E-08	58%	66%	18--65	1--48
c170L	76055--75735	107	12,611	10.91		No Hit Found									No Hit Found								
c172R	76271--76723	151	17,718	9.90		No Hit Found								1	NP_048480	a132R	59.31	3.81E-08	47%	67%	61--120	19--79
c173L	77323--76730	198	23,198	4.95		No Hit Found								1	AAK23092	hypothetical protein	67.40	2.78E-10	29%	52%	40--177	69--210
c173L														2	ZP_00811430	Methyltransferase FkbM	64.70	1.80E-09	30%	51%	43--180	114--248
c173L														3	ABA05654	methyltransferase FkbM	63.54	4.01E-09	34%	52%	59--180	116--235
c176R	78081--78329	83	9,177	10.51		No Hit Found									No Hit Found								
c178R	79120--79335	72	8,465	7.77		No Hit Found									No Hit Found								
c181L	79875--79660	72	7,514	5.54		No Hit Found									No Hit Found								
c183L	81681--80872	270	28,002	5.53		No Hit Found								1	NP_048490	a142L	172.17	1.47E-41	78%	78%	103--213	21--131
c183L														2	NP_048491	a143L	55.84	1.54E-06	89%	89%	20--47	23--50
c184L	82264--80882	461	53,389	8.44		No Hit Found								1	NP_048492	a144L	526.17	8.95E-148	57%	67%	5--461	18--473
c184L														2	T17632	hypothetical protein a141L - Chlorella virus PBCV-1	279.26	1.91E-73	60%	70%	235--461	14--240
c184L														3	NP_048495	Phe-, Gly-rich protein: RCGF 3X, GCGF 11X, RSGF 5X, GSGF 2X	60.08	1.82E-07	37%	47%	40--116	132--224
c185L	82663--82436	76	9,380	8.73		No Hit Found								1	NP_048495	Phe-, Gly-rich protein: RCGF 3X, GCGF 11X, RSGF 5X, GSGF 2X	114.78	7.74E-25	71%	82%	4--76	187--260

Gene Name	Genome Position	A.A. lenath	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to
c185L														2	NP_048492	a144L	59.31	3.86E-08	51%	64%	4--65	92--155
c186L	83049--82717	111	10,598	9.60		No Hit Found									No Hit Found							
c188R	83010--83234	75	8,439	8.43		No Hit Found									No Hit Found							
c190L	84315--83878	146	16,674	10.89		No Hit Found								1	NP_048500	contains prokaryotic membrane lipoprotein lipid attachment site	75.87	3.90E-13	53%	61%	67--143	9--85
c192L	84820--84611	70	8,351	10.54		No Hit Found									No Hit Found							
c196R	86464--86658	65	7,842	9.24		No Hit Found									No Hit Found							
c199R	87125--87364	80	8,733	4.43		No Hit Found									No Hit Found							
c201L	87976--87776	67	7,962	6.91		No Hit Found								1	NP_048515	a167L	61.23	1.01E-08	48%	62%	1--66	1--66
c205L	90993--90712	94	11,356	6.86		No Hit Found									No Hit Found							
c207R	91662--91946	95	11,440	11.54		No Hit Found								1	NP_048391	a43R	80.88	1.25E-14	54%	65%	1--75	1--75
c209L	92782--92531	84	10,068	10.74		No Hit Found									No Hit Found							
c210R	92834--93049	72	7,509	5.54		No Hit Found									No Hit Found							
c211L	93130--92852	93	11,611	11.43		No Hit Found									No Hit Found							
c213R	93448--93792	115	13,719	8.19		No Hit Found									No Hit Found							
c214R	94069--94278	70	8,428	8.40		No Hit Found									No Hit Found							
c215R	94322--94600	93	10,894	7.81		No Hit Found									No Hit Found							
c218R	95123--95371	83	10,219	11.05		No Hit Found									No Hit Found							
c219R	95277--95480	68	7,747	6.80		No Hit Found								1	NP_048601	a251aL	73.94	1.50E-12	67%	76%	1--56	83--141
c221L	96277--96062	72	8,732	12.02		No Hit Found									No Hit Found							
c222L	96690--96298	131	13,927	10.62		No Hit Found									No Hit Found							
c223L	96563--96369	65	7,794	11.02		No Hit Found									No Hit Found							
c224R	97366--97599	78	9,691	11.50		No Hit Found									No Hit Found							
c225L	97846--97577	90	10,690	5.48		No Hit Found									No Hit Found							
c226L	98073--97873	67	7,104	5.33		No Hit Found									No Hit Found							
c229L	99585--99382	68	7,374	11.50		No Hit Found									No Hit Found							
c231L	99829--99557	91	11,323	11.81		No Hit Found									No Hit Found							
c232L	100234--100004	77	9,087	8.20		No Hit Found								1	NP_048534	a187L	51.60	8.02E-06	59%	87%	1--32	216--247
c233L	101771--101568	68	7,244	12.23		No Hit Found								1	NP_048535	a188L	105.15	6.06E-22	83%	86%	1--68	5--72
c235L	102087--101800	96	11,556	8.52		No Hit Found									No Hit Found							
c237L	102706--102467	80	9,028	4.91		No Hit Found									No Hit Found							
c238R	102616--103026	137	16,220	11.53		No Hit Found									No Hit Found							
c240L	107496--107272	75	8,593	10.37		No Hit Found									No Hit Found							
c243R	108582--108794	71	8,346	8.35		No Hit Found								1	NP_048545	a198R	88.97	4.45E-17	54%	75%	1--70	5--74
c247L	110412--110158	85	10,356	9.47		No Hit Found									No Hit Found							
c248L	110609--110232	126	13,951	10.58		No Hit Found								1	NP_048548	A201L	135.96	3.23E-31	66%	79%	24--116	1--93
c249R	110539--110739	67	7,624	10.92		No Hit Found									No Hit Found							
c251L	110992--110705	96	11,788	10.16		No Hit Found									No Hit Found							
c253L	111325--111116	70	7,097	9.46		No Hit Found								1	NP_048551	a204L	125.56	4.31E-28	92%	94%	1--70	1--70
c254L	112026--111583	148	16,166	5.80		No Hit Found									No Hit Found							
c257L	112858--112664	65	7,957	9.66		No Hit Found									No Hit Found							
c258L	113487--113155	111	13,135	8.09		No Hit Found									No Hit Found							
c262R	115076--115321	82	9,540	10.65		No Hit Found									No Hit Found							
c266L	118141--117878	88	10,558	9.46		No Hit Found									No Hit Found							
c267L	118131--117883	83	9,410	11.05		No Hit Found								1	T17711	hypothetical protein a221L - Chlorella virus PBCV-1	70.09	2.14E-11	75%	88%	1--44	1--44
c268R	118076--118285	70	7,704	9.74		No Hit Found								1	NP_048570	a223R	102.06	5.10E-21	71%	78%	1--70	1--70
c269L	118757--118551	69	8,032	9.41		No Hit Found								1	NP_048572	a224L	78.57	6.06E-14	90%	92%	1--40	49--88
c273R	120301--120582	94	10,998	7.83		No Hit Found									No Hit Found							
c274L	120507--120313	65	7,395	9.43		No Hit Found									No Hit Found							
c276R	120772--120999	76	8,512	10.38		No Hit Found									No Hit Found							
c277R	121048--121383	112	12,845	7.74		No Hit Found									No Hit Found							
c278R	121413--121619	69	8,266	10.25		No Hit Found								1	NP_048580	a232R	72.79	3.32E-12	56%	73%	6--65	6--65
c279L	122093--121860	78	9,730	10.37		No Hit Found									No Hit Found							
c282L	123270--123076	65	7,071	10.86		No Hit Found									No Hit Found							
c283L	123376--123122	85	10,277	8.92		No Hit Found									No Hit Found							
c284R	123303--123560	86	10,147	11.32		No Hit Found									No Hit Found							
c287L	124418--124002	139	16,327	7.51		No Hit Found									No Hit Found							
c288R	124187--124480	98	11,601	11.21		No Hit Found									No Hit Found							
c289L	124901--124662	80	9,384	9.63		No Hit Found									No Hit Found							

Gene Name	Genome Position	A.A. length	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to
c291R	125565--125843	93	11,173	8.70		No Hit Found									No Hit Found							
c293L	126861--126511	117	13,667	5.15		No Hit Found								1	NP_048590	a242L	174.48	8.20E-43	74%	79%	1--117	1--117
c294L	127151--126864	96	10,473	10.81		No Hit Found									No Hit Found							
c295L	127574--127317	86	9,989	9.40		No Hit Found									No Hit Found							
c296L	127611--127354	86	9,966	9.45		No Hit Found									No Hit Found							
c297L	127973--127674	100	11,308	10.05		No Hit Found									No Hit Found							
c301L	131397--131020	126	15,612	10.02		No Hit Found									No Hit Found							
c302L	131285--131067	73	8,030	11.07		No Hit Found									No Hit Found							
c304R	132044--132301	86	10,130	10.16		No Hit Found									No Hit Found							
c305R	132980--133429	150	17,984	10.04		No Hit Found									No Hit Found							
c308L	134760--134509	84	10,506	9.57		No Hit Found								1	NP_048603	a252aL	90.51	1.58E-17	66%	80%	25--84	25--84
c310R	135238--135864	209	23,434	7.79		No Hit Found									No Hit Found							
c312R	135952--136152	67	7,723	9.56		No Hit Found								1	NP_048618	a264R	100.91	1.15E-20	67%	85%	1--61	1--61
c314R	136332--136652	107	11,951	10.71		No Hit Found									No Hit Found							
c316R	136926--137177	84	9,454	10.79		No Hit Found								1	NP_048624	a270R	82.03	5.62E-15	63%	67%	1--68	1--68
c317R	137108--137710	201	23,972	6.45		No Hit Found								1	NP_048626	a272R	71.63	1.50E-11	52%	74%	28--90	5--67
c320R	139175--139543	123	13,615	8.82		No Hit Found								1	NP_048635	a281R	174.48	8.29E-43	83%	85%	8--113	70--176
c322R	139561--139776	72	8,843	9.57		No Hit Found								1	NP_048633	a279R	158.69	4.56E-38	95%	95%	1--72	1--72
c323R	140657--140935	93	10,245	3.62		No Hit Found								1	NP_048634	a280R	174.10	1.05E-42	93%	93%	1--93	1--93
c325L	141664--141464	67	7,712	11.12		No Hit Found								1	NP_048637	a283L	138.27	6.49E-32	94%	97%	1--67	1--67
c326R	142606--142806	67	8,415	10.20		No Hit Found									No Hit Found							
c328L	143060--142797	88	10,735	12.19		No Hit Found									No Hit Found							
c330R	144222--144461	80	9,135	10.73		No Hit Found									No Hit Found							
c331L	144656--144390	89	11,112	12.13		No Hit Found									No Hit Found							
c332R	144409--144618	70	8,349	11.47		No Hit Found									No Hit Found							
c333R	144618--144854	79	9,404	11.24		No Hit Found									No Hit Found							
c335L	145962--145684	93	10,511	8.11		No Hit Found									No Hit Found							
c336L	146098--145880	73	8,842	11.23		No Hit Found									No Hit Found							
c338R	146527--146901	125	15,299	8.38		No Hit Found									No Hit Found							
c340L	147527--147114	138	16,602	10.27		No Hit Found								1	BAA20344	ORF245	137.50	1.09E-31	60%	74%	1--115	125--243
c341L	147342--147124	73	8,987	10.31		No Hit Found									No Hit Found							
c343R	148034--148369	112	12,380	10.29		No Hit Found								1	NP_048647	a293R	149.83	2.13E-35	73%	79%	1--102	67--168
c345R	148727--148927	67	7,924	6.08		No Hit Found									No Hit Found							
c347L	150220--149966	85	9,964	7.48		No Hit Found									No Hit Found							
c350R	151847--152107	87	10,253	8.53		No Hit Found									No Hit Found							
c352L	152482--152276	69	8,208	9.95		No Hit Found									No Hit Found							
c353L	152664--152470	65	7,404	10.57		No Hit Found									No Hit Found							
c355R	152725--152958	78	8,970	11.50		No Hit Found									No Hit Found							
c356L	153512--152814	233	27,426	7.38		No Hit Found								1	NP_048503	a155R	92.43	1.13E-17	66%	86%	16--83	27--94
c357L	153343--153101	81	9,010	9.52		No Hit Found									No Hit Found							
c359R	153869--154096	76	9,221	10.65		No Hit Found									No Hit Found							
c360R	154116--154376	87	9,662	8.83		No Hit Found									No Hit Found							
c361R	154629--154838	70	7,340	10.81		No Hit Found									No Hit Found							
c362L	155116--154841	92	10,661	11.19		No Hit Found									No Hit Found							
c364L	155750--155502	83	9,737	9.91		No Hit Found									No Hit Found							
c366R	157011--157211	67	7,781	8.41		No Hit Found								1	CAB92310	DNA methyltrasferase	64.70	9.11E-10	51%	67%	1--66	348--415
c366R														2	AAF74028	M.Hpy188I	64.70	9.11E-10	51%	67%	1--66	348--415
c368L	157552--157358	65	7,724	8.65		No Hit Found									No Hit Found							
c370L	158288--157893	132	16,358	11.06		No Hit Found									No Hit Found							
c371R	158093--158320	76	8,992	5.88		No Hit Found									No Hit Found							
c373R	158541--158852	104	12,534	7.89		No Hit Found									No Hit Found							
c375L	160225--159938	96	10,814	12.55		No Hit Found									No Hit Found							
c376L	160494--160288	69	7,990	9.44		No Hit Found									No Hit Found							
c383R	163604--163978	125	14,390	8.56		No Hit Found									No Hit Found							
c385R	164062--164265	68	8,318	9.37		No Hit Found									No Hit Found							
c388L	165204--164764	147	13,781	4.87	1	pfam05277	DUF726, Protein of unknown function (DUF726). This family consists of s	38.34	1.41E-03	45%	57%	32--120	85--161		No Hit Found							
c390R	164874--165239	122	14,249	11.34		No Hit Found									No Hit Found							
c391L	165795--165550	82	8,693	9.57		No Hit Found								1	NP_048675	a319L	148.29	6.19E-35	87%	90%	1--82	1--82
c393L	166974--166720	85	10,251	10.65		No Hit Found									No Hit Found							

Gene Name	Genome Position	A.A. lenath	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to
c394R	166963--167274	104	12,249	12.09		No Hit Found									No Hit Found								
c395L	167296--167054	81	9,032	9.53		No Hit Found									No Hit Found								
c399R	168424--168642	73	7,772	10.81		No Hit Found									No Hit Found								
c401R	169138--169344	69	7,754	9.38		No Hit Found									No Hit Found								
c402R	169430--169825	132	15,519	10.69		No Hit Found									No Hit Found								
c403L	170154--169894	87	10,415	9.01		No Hit Found									No Hit Found								
c405R	170653--170910	86	10,333	10.62		No Hit Found								1	NP_048683	a327R	79.72	2.77E-14	64%	75%	25--86	24--85
c407L	171282--171010	91	11,145	10.73		No Hit Found									No Hit Found								
c408L	171736--171488	83	9,597	8.64		No Hit Found									No Hit Found								
c409R	172546--172800	85	9,366	10.41		No Hit Found									No Hit Found								
c410R	172862--173068	69	8,172	6.46		No Hit Found									No Hit Found								
c411L	173150--172947	68	7,941	8.81		No Hit Found									No Hit Found								
c412L	173465--173232	78	9,004	4.36		No Hit Found									No Hit Found								
c416R	175246--175455	70	7,673	10.25		No Hit Found									No Hit Found								
c417R	175512--175745	78	9,550	11.08		No Hit Found									No Hit Found								
c419L	176799--176599	67	7,351	9.43		No Hit Found									No Hit Found								
c420L	177097--176882	72	8,469	4.76		No Hit Found									No Hit Found								
c421L	177102--176896	69	7,865	9.63		No Hit Found									No Hit Found								
c422R	177516--177734	73	8,106	8.19		No Hit Found									No Hit Found								
c424L	178650--178339	104	12,773	12.59		No Hit Found									No Hit Found								
c425R	178438--178758	107	12,519	7.07		No Hit Found									No Hit Found								
c426L	179432--179037	132	16,002	11.55		No Hit Found									No Hit Found								
c428R	179380--179592	71	8,587	10.24		No Hit Found									No Hit Found								
c431R	180919--181362	148	16,592	8.66		No Hit Found								1	NP_048701	a344R	143.28	2.03E-33	60%	77%	34--148	1--115
c432R	181894--182229	112	13,285	11.17		No Hit Found									No Hit Found								
c433R	182240--182512	91	10,959	11.10		No Hit Found									No Hit Found								
c436L	183172--182717	152	18,139	6.83		No Hit Found								1	NP_048704	a347L	92.05	5.29E-18	57%	72%	83--152	1--70
c441R	185762--186091	110	12,244	10.57		No Hit Found									No Hit Found								
c442R	185875--186207	111	13,069	11.06		No Hit Found									No Hit Found								
c443R	186389--186598	70	7,646	4.83		No Hit Found									No Hit Found								
c445L	186897--186688	70	7,690	12.35		No Hit Found									No Hit Found								
c446R	186739--186942	68	8,981	12.71		No Hit Found									No Hit Found								
c448R	187744--188016	91	9,560	4.77		No Hit Found									No Hit Found								
c450L	188399--188181	73	8,160	8.21		No Hit Found									No Hit Found								
c451L	188608--188411	66	8,354	8.68		No Hit Found									No Hit Found								
c452L	188952--188668	95	10,699	7.95		No Hit Found									No Hit Found								
c453L	189466--189254	71	8,352	10.01		No Hit Found									No Hit Found								
c454L	189905--189540	122	13,554	8.20		No Hit Found									No Hit Found								
c455L	190553--190311	81	8,974	4.64		No Hit Found									No Hit Found								
c456L	190890--190396	165	19,722	9.86		No Hit Found									No Hit Found								
c457L	191383--191150	78	9,128	7.98		No Hit Found									No Hit Found								
c458L	191654--191370	95	10,029	3.14		No Hit Found									No Hit Found								
c460R	191923--192192	90	10,868	10.95		No Hit Found									No Hit Found								
c461R	192227--192478	84	9,664	8.22		No Hit Found									No Hit Found								
c463R	192330--192695	122	15,030	10.78		No Hit Found								1	NP_048724	a367R	69.32	3.64E-11	41%	49%	1--91	1--91
c464R	192682--192903	74	8,075	3.54		No Hit Found									No Hit Found								
c465R	193494--193793	100	11,295	12.65		No Hit Found								1	NP_048734	a377R	86.27	2.92E-16	55%	63%	14--100	6--91
c468R	194418--194948	177	20,563	11.10		No Hit Found								1	NP_048737	a380R	144.05	1.77E-33	71%	82%	49--149	1--101
c469R	194668--194871	68	7,734	11.11		No Hit Found								1	NP_048738	a381R	127.49	1.14E-28	89%	91%	1--68	9--76
c471L	195563--195276	96	10,916	8.81		No Hit Found									No Hit Found								
c472L	195962--195699	88	9,947	12.15		No Hit Found									No Hit Found								
c473L	196443--196084	120	14,174	8.04		No Hit Found									No Hit Found								
c474L	197139--196792	116	12,847	10.36		No Hit Found								1	NP_048742	a385L	59.31	3.86E-08	85%	85%	35--69	1--35
c476R	196916--197356	147	17,664	12.63		No Hit Found								1	NP_048743	Gly-rich, AGLG (9x); similar to herpesvirus hypothetical protein 5, corresp	61.62	7.82E-09	80%	80%	61--96	57--92
c477R	197986--198198	71	8,501	11.94		No Hit Found								1	NP_048745	a388R	50.83	1.34E-05	78%	78%	2--33	40--71
c478R	198384--198680	99	11,302	10.98		No Hit Found								1	NP_048748	a391R	146.36	2.39E-34	76%	77%	1--99	1--95
c480L	199076--198861	72	8,047	6.73		No Hit Found									No Hit Found								
c481R	199524--199727	68	7,583	6.49		No Hit Found									No Hit Found								

Gene Name	Genome Position	A.A. lenath	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to
c482L	199906--199709	66	8,079	6.08		No Hit Found									No Hit Found								
c488R	202540--202737	66	7,352	5.69		No Hit Found									No Hit Found								
c489R	202826--203029	68	8,180	8.38		No Hit Found									No Hit Found								
c495L	205972--205670	101	10,913	4.64		No Hit Found									No Hit Found								
c499L	207957--207397	187	19,795	13.59		No Hit Found									No Hit Found								
c500L	208594--208388	69	7,216	4.54		No Hit Found									No Hit Found								
c501L	208895--209098	68	9,523	11.30		No Hit Found									No Hit Found								
c502R	209135--208896	80	7,695	10.89		No Hit Found									No Hit Found								
c505R	210028--210228	67	7,716	8.19		No Hit Found								1	NP_048712	a355L	69.71	2.83E-11	59%	62%	2--65	14--70
c506R	210244--210450	69	8,191	7.34		No Hit Found									No Hit Found								
c508R	211235--211603	123	13,737	10.64		No Hit Found								1	NP_048766	a409R	73.94	1.52E-12	82%	86%	1--46	37--82
c511L	212597--212268	110	12,766	10.20		No Hit Found									No Hit Found								
c514R	213721--213972	84	9,652	8.82		No Hit Found									No Hit Found								
c516R	214835--215071	79	8,394	10.76		No Hit Found									No Hit Found								
c517R	215109--215402	98	9,869	6.50		No Hit Found									No Hit Found								
c520R	216571--216768	66	8,038	7.12		No Hit Found									No Hit Found								
c524L	218761--218330	144	17,685	6.94		No Hit Found									No Hit Found								
c525L	218547--218350	66	7,822	7.78		No Hit Found									No Hit Found								
c526R	218409--218711	101	11,774	10.92		No Hit Found									No Hit Found								
c530R	219598--219834	79	10,083	12.42		No Hit Found									No Hit Found								
c533R	222712--222963	84	10,680	11.63		No Hit Found									No Hit Found								
c534L	222970--222776	65	7,619	4.64		No Hit Found									No Hit Found								
c536R	223213--223422	70	7,946	11.50		No Hit Found									No Hit Found								
c541R	224827--225084	86	10,233	11.09		No Hit Found									No Hit Found								
c544R	225889--226092	68	8,318	10.15		No Hit Found								1	NP_048799	a442R	74.33	1.15E-12	47%	70%	1--65	2--66
c548L	228137--227904	78	8,991	8.19		No Hit Found									No Hit Found								
c549L	228274--228053	74	9,185	12.38		No Hit Found									No Hit Found								
c550R	228515--228820	102	11,578	10.84		No Hit Found									No Hit Found								
c552R	228980--229195	72	7,853	9.49		No Hit Found								1	NP_048803	a446R	102.45	3.88E-21	89%	91%	17--72	1--56
c553R	229460--229654	65	7,222	11.63		No Hit Found								1	NP_048804	a447R	126.72	1.97E-28	95%	98%	1--65	35--99
c555L	230640--230437	68	8,309	9.20		No Hit Found									No Hit Found								
c557L	231355--231155	67	7,965	8.72		No Hit Found									No Hit Found								
c561R	233698--233922	75	8,478	5.50		No Hit Found								1	NP_048810	a453R	88.58	5.96E-17	64%	66%	1--75	15--89
c563R	234730--235155	142	15,769	11.78		No Hit Found								1	NP_048814	a457R	115.16	5.90E-25	78%	80%	32--107	1--76
c564L	235249--235001	83	10,029	11.39		No Hit Found								1	NP_048815	a458L	107.07	1.58E-22	60%	74%	1--83	1--83
c565R	235008--235334	109	13,234	6.23		No Hit Found									No Hit Found								
c566R	235497--235772	92	10,922	10.74		No Hit Found									No Hit Found								
c567R	235840--236046	69	7,712	11.10		No Hit Found									No Hit Found								
c572R	239382--239621	80	9,499	5.58		No Hit Found									No Hit Found								
c574L	241380--241135	82	8,847	9.44		No Hit Found								1	NP_048825	a469L	54.30	1.22E-06	42%	52%	8--82	3--76
c576R	242004--242207	68	8,156	12.37		No Hit Found									No Hit Found								
c578L	243006--242806	67	7,615	7.28		No Hit Found									No Hit Found								
c581R	244422--244925	168	20,013	9.69		No Hit Found								1	NP_048835	Phe-rich	63.16	3.42E-09	34%	36%	1--107	1--107
c582L	244885--244649	79	9,482	12.03		No Hit Found									No Hit Found								
c585R	245549--245776	76	8,634	8.17		No Hit Found									No Hit Found								
c589L	247798--247472	109	12,914	6.61		No Hit Found									No Hit Found								
c591L	248180--247986	65	7,590	8.15		No Hit Found									No Hit Found								
c592L	248677--248378	100	11,404	10.13		No Hit Found									No Hit Found								
c594L	248861--248628	78	9,004	8.82		No Hit Found									No Hit Found								
c598R	250572--250826	85	9,909	9.04		No Hit Found									No Hit Found								
c599L	251481--251077	135	14,606	10.36		No Hit Found								1	NP_048854	Pro-rich, IPPPNMSLPLS (3x)	108.61	5.50E-23	52%	52%	1--120	1--120
c601L	251366--251136	77	9,761	8.11		No Hit Found								1	NP_048855	a499L	56.23	3.26E-07	88%	92%	1--27	1--27
c603R	251958--252380	141	12,711	9.35		No Hit Found									No Hit Found								
c606R	253462--253725	88	10,755	8.05		No Hit Found								1	NP_048860	a504R	176.79	1.65E-43	90%	95%	1--87	1--87
c607L	253954--253745	70	8,193	10.53		No Hit Found									No Hit Found								
c609R	254024--254254	77	9,572	8.82		No Hit Found									No Hit Found								
c610R	254295--254501	69	8,436	11.12		No Hit Found								1	NP_048863	a507R	87.43	1.30E-16	60%	78%	1--65	3--67
c611R	254634--254846	71	8,705	11.52		No Hit Found								1	NP_048863	a507R	77.80	1.03E-13	57%	71%	1--71	116--186

Gene Name	Genome Position	A.A. lenath	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession		BLASTp Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to
c612R	255250--255477	76	8,867	10.98		No Hit Found								1	NP_048866	a510R		93.59	1.85E-18	89%	92%	13--67	2--56
c614L	256042--255743	100	11,629	11.36		No Hit Found									No Hit Found								
c617R	256457--256780	108	13,055	3.84		No Hit Found									No Hit Found								
c623R	260350--260727	126	14,999	10.45		No Hit Found									No Hit Found								
c625R	260645--260917	91	10,217	4.48		No Hit Found								1	NP_048503	a155R		83.57	1.88E-15	61%	79%	16--82	27--93
c626R	261053--261349	99	12,307	11.85		No Hit Found									No Hit Found								
c628R	261949--262200	84	9,930	6.00		No Hit Found									No Hit Found								
c631L	262842--262534	103	11,102	6.48		No Hit Found								1	NP_048874	a518R		123.64	1.63E-27	64%	72%	1--98	3--100
c631L														2	NP_048885	a529L		112.85	2.88E-24	86%	88%	31--97	1--67
c631L														3	NP_049041	a685R		52.37	4.62E-06	53%	59%	46--97	15--66
c633L	263400--263116	95	10,738	7.34		No Hit Found									No Hit Found								
c637R	265541--265768	76	9,000	8.21		No Hit Found									No Hit Found								
c639L	267680--267480	67	7,432	11.01		No Hit Found									No Hit Found								
c640R	267684--267893	70	7,788	8.08		No Hit Found									No Hit Found								
c642R	268730--268954	75	9,167	10.45		No Hit Found									No Hit Found								
c646R	269556--269795	80	8,610	11.46		No Hit Found									No Hit Found								
c647R	270148--270354	69	8,068	10.67		No Hit Found									No Hit Found								
c649R	270408--270824	139	15,586	10.08		No Hit Found									No Hit Found								
c650R	270560--270859	100	12,308	8.19		No Hit Found									No Hit Found								
c653R	272131--272412	94	10,313	4.45		No Hit Found									No Hit Found								
c654R	272479--272742	88	9,942	7.69		No Hit Found									No Hit Found								
c655R	273079--273276	66	7,138	4.14		No Hit Found								1	NP_048897	a541R		59.69	2.94E-08	51%	62%	3--66	34--96
c656R	274303--274548	82	8,845	4.71		No Hit Found									No Hit Found								
c657L	275164--274937	76	9,244	11.55		No Hit Found									No Hit Found								
c659L	276357--275908	150	17,931	8.50		No Hit Found									No Hit Found								
c660L	276176--275958	73	8,154	10.82		No Hit Found								1	NP_048901	a545L		132.11	4.74E-30	87%	91%	1--73	1--73
c662R	277646--277912	89	10,287	5.06		No Hit Found									No Hit Found								
c664R	278090--278368	93	10,919	6.62		No Hit Found								1	NP_048905	a549R		74.33	1.14E-12	41%	62%	1--80	1--80
c665R	278744--278977	78	9,229	6.35		No Hit Found								1	NP_048906	a550R		77.80	1.04E-13	44%	74%	1--78	55--132
c666R	279068--279433	122	14,344	6.84		No Hit Found									No Hit Found								
c668L	280152--279628	175	21,526	9.79		No Hit Found									No Hit Found								
c671R	280659--281009	117	13,112	10.68		No Hit Found									No Hit Found								
c672R	280985--281263	93	10,824	8.37		No Hit Found								1	NP_048911	a555R		168.32	5.78E-41	89%	91%	1--93	1--93
c673R	281654--281881	76	8,378	8.06		No Hit Found									No Hit Found								
c674L	282272--282066	69	7,971	10.96		No Hit Found									No Hit Found								
c677R	283694--284077	128	14,105	6.98		No Hit Found								1	NP_048916	a560R		72.79	3.33E-12	65%	75%	3--62	45--104
c679R	284289--284639	117	13,356	4.85		No Hit Found									No Hit Found								
c680R	284566--284850	95	10,558	7.72		No Hit Found									No Hit Found								
c682R	285472--285705	78	9,588	11.24		No Hit Found									No Hit Found								
c683R	285888--286115	76	8,753	7.57		No Hit Found								1	NP_048922	a566L		95.13	6.35E-19	95%	95%	35--76	49--90
c684L	286278--286030	83	9,586	12.35		No Hit Found									No Hit Found								
c686L	288667--288263	135	15,524	7.64		No Hit Found								1	NP_048922	a566L		168.70	4.48E-41	88%	88%	1--88	1--90
c689R	290040--290249	70	8,717	8.45		No Hit Found									No Hit Found								
c692L	291082--290816	89	10,577	8.53		No Hit Found									No Hit Found								
c695R	291831--292052	74	8,008	6.65		No Hit Found									No Hit Found								
c697L	292684--292448	79	8,679	10.91		No Hit Found								1	NP_048874	a518R		64.31	1.19E-09	53%	66%	17--78	1--62
c700R	294008--294205	66	7,959	8.96		No Hit Found									No Hit Found								
c702R	294495--294737	81	10,045	12.26		No Hit Found									No Hit Found								
c703L	295008--294775	78	9,649	11.87		No Hit Found								1	NP_048938	a582L		122.87	2.82E-27	78%	85%	1--78	1--78
c704R	295166--295399	78	9,098	11.65		No Hit Found									No Hit Found								
c706R	295636--295863	76	8,209	9.61		No Hit Found									No Hit Found								
c708R	296776--297015	80	9,519	4.84		No Hit Found									No Hit Found								
c709R	297878--298177	100	11,570	11.19		No Hit Found									No Hit Found								
c710R	298147--298341	65	7,526	7.53		No Hit Found								1	NP_048943	a587R		112.08	5.01E-24	80%	89%	1--65	1--65
c711R	298310--298549	80	8,692	12.12		No Hit Found									No Hit Found								
c712R	298822--299517	232	26,620	5.51		No Hit Found								1	NP_048944	a588R		109.38	8.85E-23	50%	68%	1--116	1--116
c713R	299039--299362	108	12,116	10.65		No Hit Found									No Hit Found								
c716L	301023--300682	114	11,519	7.30		No Hit Found								1	NP_048951	a595L		65.86	4.16E-10	62%	68%	1--59	19--82
c717R	300930--301148	73	8,461	11.74		No Hit Found									No Hit Found								

Gene Name	Genome Position	A.A. lenath	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identitv	% Positive	Query from-to	Hit from-to
c720R	301999--302544	182	21,575	6.23		No Hit Found									No Hit Found							
c721R	302351--302581	77	8,832	10.50		No Hit Found								1	NP_048956	a600R	95.52	4.85E-19	67%	75%	3--76	11--81
c724L	303571--303308	88	10,598	5.09		No Hit Found									No Hit Found							
c730R	306186--306458	91	10,984	9.52		No Hit Found								1	NP_048966	a610R	173.71	1.38E-42	89%	89%	1--91	1--91
c732R	307630--307887	86	9,951	6.95		No Hit Found									No Hit Found							
c734R	308977--309249	91	9,847	9.69		No Hit Found								1	NP_048972	a616R	116.32	2.62E-25	62%	67%	2--91	4--93
c738R	310936--311184	83	9,070	5.59		No Hit Found									No Hit Found							
c743R	313791--314033	81	10,084	11.26		No Hit Found									No Hit Found							
c746L	315067--314846	74	8,396	10.19		No Hit Found								1	NP_048982	a626L	164.85	6.57E-40	100%	100%	1--74	1--74
c749R	317565--317786	74	8,495	11.36		No Hit Found								1	NP_048986	a630R	95.13	6.39E-19	67%	67%	1--74	1--74
c750R	317883--318134	84	9,368	10.23		No Hit Found									No Hit Found							
c751L	318217--317990	76	8,645	9.54		No Hit Found									No Hit Found							
c752R	319348--319650	101	11,949	9.40		No Hit Found									No Hit Found							
c758L	321419--321105	105	12,528	4.79		No Hit Found									No Hit Found							
c760L	321983--321588	132	14,744	9.00		No Hit Found								1	NP_048995	a639L	250.37	1.19E-65	95%	96%	1--132	1--132
c761R	321812--322048	79	8,848	11.89		No Hit Found								1	NP_048996	a640R	152.14	4.33E-36	94%	97%	1--79	1--79
c762L	322373--322119	85	9,710	11.11		No Hit Found								1	NP_048997	a641L	168.32	5.94E-41	96%	97%	1--85	1--85
c764L	323418--323110	103	11,914	11.57		No Hit Found									No Hit Found							
c768R	325179--325496	106	12,145	7.92		No Hit Found									No Hit Found							
c769L	325587--325351	79	9,349	11.86		No Hit Found								1	NP_049011	a655L	73.17	2.56E-12	57%	70%	9--78	1--70
c770R	325499--325759	87	11,038	11.44		No Hit Found									No Hit Found							
c775R	327489--327767	93	43,880	8.00		No Hit Found									No Hit Found							
c776R	327685--327906	74	8,238	4.18		No Hit Found								1	NP_048503	a155R	84.34	1.13E-15	66%	76%	5--73	18--84
c777L	328022--327756	89	9,671	10.81		No Hit Found									No Hit Found							
c778R	327854--328186	111	12,186	8.25		No Hit Found									No Hit Found							
c779L	328307--328026	94	11,341	12.45		No Hit Found								1	NP_048504	a156L	56.61	2.44E-07	39%	59%	6--93	19--107
c780L	328556--328332	75	8,562	12.23		No Hit Found									No Hit Found							
c782L	329124--328930	65	7,536	7.92		No Hit Found									No Hit Found							
c784R	329322--329543	74	8,289	8.07		No Hit Found									No Hit Found							
c786R	330130--330351	74	8,035	10.78		No Hit Found									No Hit Found							
c787R	330745--331128	128	14,130	7.85		No Hit Found									No Hit Found							
c789R	332984--333271	96	11,065	7.85		No Hit Found								1	NP_049023	similar to Chlorella virus CVK2 unknown ORF, corresponds to GenBank A	189.12	3.24E-47	91%	97%	1--96	1--96
c790R	333374--333568	65	7,433	7.72		No Hit Found								1	NP_049024	similar to Chlorella virus CVK2 unknown ORF, corresponds to GenBank A	125.18	5.72E-28	87%	93%	1--65	1--65
c791R	333483--333698	72	8,040	11.46		No Hit Found								1	NP_049025	similar to Chlorella virus CVK2 unknown ORF, corresponds to GenBank A	149.83	2.12E-35	100%	100%	1--72	12--83
c792R	334913--335278	122	14,173	9.90		No Hit Found								1	NP_049026	similar to Chlorella virus CVK2 unknown ORF, corresponds to GenBank A	223.79	1.16E-57	87%	92%	1--122	1--122
c794L	336130--335867	88	10,592	4.66		No Hit Found									No Hit Found							
c795R	336125--336397	91	10,499	11.12		No Hit Found									No Hit Found							
c797R	336198--336527	110	13,279	10.96		No Hit Found								1	NP_048630	similar to PBCV-1 ORF a80L, corresponds to GenBank Accession Numbe	59.31	3.82E-08	48%	66%	49--110	3--64
c799L	337668--337270	133	14,418	6.65		No Hit Found								1	NP_049033	a677L	115.16	5.93E-25	76%	82%	1--69	1--75
c801R	339024--339272	83	9,941	7.92		No Hit Found									No Hit Found							
c803R	339346--339963	206	23,724	7.94		No Hit Found								1	NP_048354	a6L	67.40	3.02E-10	47%	67%	74--143	1--71
c804R	339521--339748	76	8,121	9.74		No Hit Found									No Hit Found							
c805R	340292--340516	75	8,658	4.17		No Hit Found									No Hit Found							
c807R	340362--340592	77	8,449	10.19		No Hit Found									No Hit Found							
c808R	340919--341197	93	10,890	10.90		No Hit Found									No Hit Found							
c810R	341935--342282	116	13,092	5.54		No Hit Found								1	NP_048354	a6L	57.38	1.47E-07	51%	72%	40--86	1--47
c811L	342680--342471	70	8,233	5.13		No Hit Found									No Hit Found							
c812R	342546--342746	67	7,515	7.18		No Hit Found								1	NP_049046	identical to PBCV-1 terminal repeat ORF, corresponds to GenBank Acces	58.54	6.53E-08	50%	68%	1--60	12--66
c813L	343070--342846	75	8,636	6.66		No Hit Found									No Hit Found							
c814L	343967--343539	143	16,443	10.82		No Hit Found									No Hit Found							